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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/492,028

DATE: 09/27/2000  
TIME: 15:37:23

Input Set : A:\Uc-926-1.app  
Output Set: N:\CRF3\09272000\I492028.raw

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3 <110> APPLICANT: Zuker, Charles S.  
4 The Regents of the University of California  
6 <120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell  
7 Specific G-Protein Alpha Subunit  
9 <130> FILE REFERENCE: 02307E-092610US  
11 <140> CURRENT APPLICATION NUMBER: US 09/492,028  
12 <141> CURRENT FILING DATE: 2000-01-26  
14 <150> PRIOR APPLICATION NUMBER: US 60/117,367  
15 <151> PRIOR FILING DATE: 1999-01-27  
17 <160> NUMBER OF SEQ ID NOS: 2  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 1503  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Mus sp.  
26 <220> FEATURE:  
27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (157)..(1224)  
29 <223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14  
30 subunit (TC-Galpha14)  
32 <400> SEQUENCE: 1  
33 aactgccttc gagaagcggtt agccatagaga tccgagccctc ttctccatac catatgttgt 60  
35 tcaggtgggtt tcctcttcaa accttgcgtc tgccgataat ccgcgcggcc gggcgtaag 120  
37 ctccaggatcc ctgtcgatcc gtcgagggtgg caagcc atg gcc ggc tgc tgc tgt 174  
38 Met Ala Gly Cys Cys Cys  
39 1 5  
41 ttg tct gcg gag gag aaa gag tct cag cgc atc agc gcg gag atc gag 222  
42 Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu  
43 10 15 20  
45 cgg cac gtt cgc cgc gac aag aag gac gac gcg cgc cgg gag ctc aag ctg 270  
46 Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu  
47 25 30 35  
49 ctg ttg ctg gga acc ggt gag agt ggg aaa agc acc ttt atc aag cag 318  
50 Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln  
51 40 45 50  
53 atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc 366  
54 Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly  
55 55 60 65 70  
57 ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg 414  
58 Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met  
59 75 80 85  
61 atc aga gca atg gat acc ctg agg ata caa tac atg tgt gag cag aat 462  
62 Ile Arg Ala Met Asp Thr Leu Arg Ile Gln Tyr Met Cys Glu Gln Asn  
63 90 95 100  
65 aag gaa aat gcc cag atc acc agg gaa gtg gaa gta gac aag gtc act 510  
66 Lys Glu Asn Ala Gln Ile Ile Arg Glu Val Glu Val Asp Lys Val Thr  
67 105 110 115

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69 gca ctc tct aga gac cag gtg gca gcc atc aag cag ctg tgg ctg gat 558  
 70 Ala Leu Ser Arg Asp Gln Val Ala Ala Ile Lys Gln Leu Trp Leu Asp  
 71 120 125 130  
 73 ccc gga atc cag gag tgt tac gac agg agg agg gag tac cag ctg tca 606  
 74 Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser  
 75 135 140 145 150  
 77 gac tct gcc aaa tat tac ctg acg gac att gag cgt atc gcc atg ccc 654  
 78 Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile Glu Arg Ile Ala Met Pro  
 79 155 160 165  
 81 tct ttc gtg cca aca caa cag gat gtg ctt cgt gtt aga gtg ccc acc 702  
 82 Ser Phe Val Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr  
 83 170 175 180  
 85 act ggc atc ata gaa tat cca ttc gac ctg gaa aac atc atc ttc cga 750  
 86 Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg  
 87 185 190 195  
 89 atg gtg gat gtt ggt ggc cag cga tct gaa cga cgg aaa tgg att cac 798  
 90 Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His  
 91 200 205 210  
 93 tgc ttt gag agt gtc acc tcc atc att ttc ttg gtt gct ctg agt gaa 846  
 94 Cys Phe Glu Ser Val Thr Ser Ile Ile Phe Leu Val Ala Leu Ser Glu  
 95 215 220 225 230  
 97 tat gac cag gtt ctg gct gag tgt gac aat gag aac cgc atg gag gag 894  
 98 Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn Glu Asn Arg Met Glu Glu  
 99 235 240 245  
 101 agc aaa gcc ctg ttt aga acc atc acc tac ccc tgg ttt ctg aac 942  
 102 Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Leu Asn  
 103 250 255 260  
 105 tcc tcc gtg att ctg ttc tta aac aag aag gat ctt cta gag gag aaa 990  
 106 Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys  
 107 265 270 275  
 109 atc atg tac tct cat cta att agc tac ttc cca gag tac aca gga cca 1038  
 110 Ile Met Tyr Ser His Leu Ile Ser Tyr Phe Pro Glu Tyr Thr Gly Pro  
 111 280 285 290  
 113 aag caa gat gtc aaa gcg gcc agg gac ttt atc ctg aag ctg tat caa 1086  
 114 Lys Gln Asp Val Lys Ala Ala Arg Asp Phe Ile Leu Lys Leu Tyr Gln  
 115 295 300 305 310  
 117 gac cag aat cct gac aaa gag aag gtt atc tat tct cac ttc act tgt 1134  
 118 Asp Gln Asn Pro Asp Lys Glu Lys Val Ile Tyr Ser His Phe Thr Cys  
 119 315 320 325  
 121 gct aca gac acc gag aat atc cgc ttt gtg ttt gct gct gtc aaa gac 1182  
 122 Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp  
 123 330 335 340  
 125 aca atc cta cag cta aac cta cgg gag ttc aac ttg gtg taa 1224  
 126 Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe Asn Leu Val  
 127 345 350 355  
 129 atggaggggcc tactcctccg agacagaggg tgatctgagc cttccctgcc tgatctacaa 1284  
 131 gtgccttctgg accaggacctt aaggacattta tgtagccac aggacagaga tggtagtgc 1344  
 133 aatgtaaaa atacccacc aaccctttta agtgttta attcttact gtctaactct 1404  
 135 tttctcgct tttgggttcaa cgattagta tcattttga gtgggtcccc ctctccattt 1464

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137 tttttaaact agtggtaaac agtttattaaa aatcatgc 1503  
 140 <210> SEQ ID NO: 2  
 141 <211> LENGTH: 355  
 142 <212> TYPE: PRT  
 143 <213> ORGANISM: Mus sp.  
 145 <400> SEQUENCE: 2  
 146 Met Ala Gly Cys Cys Cys Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg  
 147 1 5 10 15  
 148 Ile Ser Ala Glu Ile Glu Arg His Val Arg Arg Asp Lys Lys Asp Ala  
 149 20 25 30  
 150 Arg Arg Glu Leu Lys Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys  
 151 35 40 45  
 152 Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser  
 153 50 55 60  
 154 Asp Glu Asp Arg Lys Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe  
 155 65 70 75 80  
 156 Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Arg Ile Gln  
 157 85 90 95  
 158 Tyr Met Cys Glu Gln Asn Lys Glu Asn Ala Gln Ile Ile Arg Glu Val  
 159 100 105 110  
 160 Glu Val Asp Lys Val Thr Ala Leu Ser Arg Asp Gln Val Ala Ala Ile  
 161 115 120 125  
 162 Lys Gln Leu Trp Leu Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg  
 163 130 135 140  
 164 Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile  
 165 145 150 155 160  
 166 Glu Arg Ile Ala Met Pro Ser Phe Val Pro Thr Gln Gln Asp Val Leu  
 167 165 170 175  
 168 Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu  
 169 180 185 190  
 170 Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu  
 171 195 200 205  
 172 Arg Arg Lys Trp Ile His Cys Phe Glu Ser Val Thr Ser Ile Ile Phe  
 173 210 215 220  
 174 Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn  
 175 225 230 235 240  
 176 Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr  
 177 245 250 255  
 178 Tyr Pro Trp Phe Leu Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys  
 179 260 265 270  
 180 Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Ile Ser Tyr Phe  
 181 275 280 285  
 182 Pro Glu Tyr Thr Gly Pro Lys Gln Asp Val Lys Ala Ala Arg Asp Phe  
 183 290 295 300  
 184 Ile Leu Lys Leu Tyr Gln Asp Gln Asn Pro Asp Lys Glu Lys Val Ile  
 185 305 310 315 320  
 186 Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val  
 187 325 330 335  
 188 Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe

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189	340	345	350
190	Asn Leu Val		
191	355		

VERIFICATION SUMMARY  
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Input Set : A:\Uc-926-1.app  
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